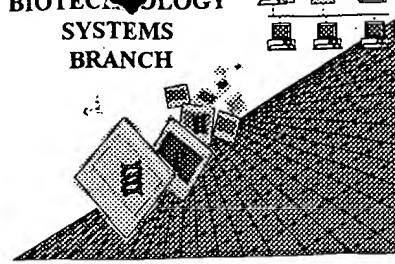


## RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/828,995  
Source: O1PE  
Date Processed by STIC: 4/30/2001

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

**FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.**

**FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.**

**PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:**

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be down loaded from the USPTO website at the following address:**  
**<http://www.uspto.gov/web/offices/pac/checker>**

# Raw Sequence Listing Error Summary

## ERROR DETECTED    SUGGESTED    CORRECTION

SERIAL NUMBER: 09/828,995

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1  Wrapped Nucleic    The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".

2  Wrapped Aminos    The amino acid number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".

3  Incorrect Line Length    The rules require that a line not exceed 72 characters in length. This includes spaces.

4  Misaligned Amino Acid Numbering    The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5  Non-ASCII    This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6  Variable Length    Sequence(s) \_\_\_\_\_ contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.

7  PatentIn ver. 2.0 "bug"    A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

8  Skipped Sequences (OLD RULES)    Sequence(s) \_\_\_\_\_ missing. If intentional, please use the following format for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X:  
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:  
This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9  Skipped Sequences (NEW RULES)    Sequence(s) \_\_\_\_\_ missing. If intentional, please use the following format for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000

10  Use of n's or Xaa's (NEW RULES)    Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11  Use of "Artificial" (NEW RULES)    Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.  
Valid response is Artificial Sequence.

12  Use of <220>Feature (NEW RULES)    Sequence(s) \_\_\_\_\_ are missing the <220>Feature and associated headings.  
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"  
Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)

13  PatentIn ver. 2.0 "bug"    Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.

OIPE

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/828,995

DATE: 04/30/2001  
TIME: 09:06:25

Input Set : A:\A1-71.app  
Output Set: N:\CRF3\04302001\I828995.raw

Does Not Comply  
Corrected Diskette Needed

3 <110> APPLICANT: McCall, Catherine A.  
4 Tang, Liang  
5 Heska Corporation  
7 <120> TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATED TO CANINE IgG AND  
8 CANINE IL-13 RECEPTORS  
10 <130> FILE REFERENCE: AL-7  
OK> 12 <140> CURRENT APPLICATION NUMBER: US/09/828,995  
13 <141> CURRENT FILING DATE: 2001-04-09  
15 <150> PRIOR APPLICATION NUMBER: 60/195,659  
16 <151> PRIOR FILING DATE: 2000-04-07  
18 <150> PRIOR APPLICATION NUMBER: 60/195,874  
19 <151> PRIOR FILING DATE: 2000-04-07  
21 <160> NUMBER OF SEQ ID NOS: 104  
23 <170> SOFTWARE: PatentIn Ver. 2.1

## ERRORED SEQUENCES

2874 <210> SEQ ID NO: 59  
2875 <211> LENGTH: 878  
2876 <212> TYPE: DNA  
2877 <213> ORGANISM: Canis familiaris  
2879 <400> SEQUENCE: 59  
E--> 2880 tttttttttt tttttttt taaaataaga tttattcaat atttgaggaa aagtttcagt 60  
2881 ttaataagac tcatatattaa catctggcca taagactgaa agttactgag tcaacagaat 120  
2882 gtgtcttgcgtat gaaaaagac ttctttttt gtatgaaaga tcgttttcag taaaggccctt 180  
2883 tgcttataaca aaagcaggca agttattacc aaaacaaaata ttgagacaaa agcaaatgg 240  
2884 atcaagaaaa atactaaggat ttccttccat atgtcaccc tccagcattt gttatcactt 300  
2885 cactcactcc agattccatc atctgagccaa taaatattca ctttacttct taccaaaaag 360  
2886 cataattttt ggctttcatt tgatgttctt gtgatttgc tctcatttc aactgtggta 420  
2887 gtcacccaag tagtaccatc ctctgtgaat tcaatttcat aaatgaaaca ttggctgga 480  
2888 atgggtcctt taggcatgtt ccatttcagg ttaatttcctt ctgaatttctt cacagtaaga 540  
2889 ctaaggtatg ctggggcat aggttaact atatttgaa gctaaaaat aaaaatgcgt 600  
2890 ggtctgatag gctgggattc tgatgaccca ttaacacaga tttatgtct 660  
2891 gatgactcca aatagggaaa cctgcattcc atattttc cattaacctt gatgtaatca 720  
2892 gtacactctg ctgaatggtc caagccctca taccagtaaa acaactggtt atggatca 780  
2893 aaatggacac ccatgccagg tttccaagag cagactaaat attgccagtt gtaatataca 840  
2894 cagtcacat cttgaatttt agttcccgaa tttccctt 878

PYS

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/828,995

DATE: 04/30/2001  
TIME: 09:06:27

Input Set : A:\A1-71.app  
Output Set: N:\CRF3\04302001\I828995.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:701 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16  
L:956 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:18  
L:956 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:18  
L:956 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18  
L:1317 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25  
L:1318 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25  
L:1326 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25  
L:1386 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:26  
L:1386 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:26  
L:1386 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:26  
L:1386 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26  
L:1389 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:26  
L:1389 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:26  
L:1389 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:26  
L:1389 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26  
L:1422 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:27  
L:1422 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:27  
L:1422 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27  
L:1482 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28  
L:1484 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28  
L:1534 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:30  
L:1534 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:30  
L:1534 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30  
L:1535 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:30  
L:1535 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:30  
L:1535 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30  
L:2204 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:40  
L:2204 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:40  
L:2204 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40  
L:2314 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:48  
L:2314 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:48  
L:2314 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:48  
L:2814 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:57  
L:2880 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:59  
L:3016 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:60  
L:3114 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:62  
L:3114 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:62  
L:3114 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:62  
L:4829 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:83  
L:4829 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:83  
L:4829 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:83  
L:4845 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:84  
L:4845 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:84  
L:4845 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:84  
L:4861 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:85  
L:4861 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:85  
L:4861 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:85

## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/828,995

DATE: 04/30/2001

TIME: 09:06:27

Input Set : A:\Al-71.app  
Output Set: N:\CRF3\04302001\I828995.raw

L:4877 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:86  
L:4877 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:86  
L:4877 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:86  
L:4893 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:87  
L:4893 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:87  
L:4893 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:87  
L:4909 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:88  
L:4909 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:88  
L:4909 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:88